

8/22/06

ZM

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	24	thomas.in. and gardella.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:51
L2	22	henry.in. and kronenberg.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:51
L3	163	potts.in. and john.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:52
L4	183	I1 or I2 or I3	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:52
L5	35	I4 and parathyroid	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:53
L6	23	L5 and (truncat\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:53
L7	6	L5 and ((truncat\$4) same extracellular)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:56
L8	1	I4 and hdelnt\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:56
L10	3	I4 and (hdelnt\$4 or delnt\$4 or hdel-nt\$4 or h-delnt\$4 or h-del-nt\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:57

EAST Search History

L11	0	I4 and E1-G\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:57
L12	0	I4 and E1G\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:58
L13	0	I4 and delta-nt\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:58
L14	0	I4 and r-delta-nt\$4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 11:58
L17	32	(gardella.in. or kronenberg.in. or potts.in.) and (parathyroid)	FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:10
L18	21	(gardella.in. or kronenberg.in. or potts.in.) and (parathyroid) and receptor	FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:11
L19	0	(r-delta-e1\$4 or rdelta-e1\$4 or rdeltae1\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:12
L20	1	26-181	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:12
L21	287	(residue near5 "26") and (residue near5 "181")	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:13
L22	35	(residue near5 "26") same (residue near5 "181")	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:13

EAST Search History

L23	16	(residue near5 "26") same (residue near5 "181") and parathyroid	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:17
L24	14	(residue near5 "26") same (residue near5 "181") and (parathyroid same receptor)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:17
L25	1	(r-delta-nt\$4 or rdeltant\$4 or rdelta-nt\$4) or (r adj delta adj nt\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:22
L26	84	(pth.ti. or parathyroid.ti.) and receptor.ti.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:21
L27	282	(parathyroid adj hormone adj receptor) or (pth adj receptor) same (agonist or antagonist)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L28	110	((parathyroid adj hormone adj receptor) or (pth adj receptor)) same (agonist or antagonist)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L29	11	"20030144209".pn. or "20030162256".pn. or "20030166838".pn. or "6803213".pn. or "20050026839".pn. or "4086196".pn. or "5217896".pn. or "6417333".pn. or "6495662".pn. or "6537965".pn. or "6541220".pn.	US-PGPUB; USPAT	OR	ON	2006/08/22 12:23
L30	449	(parathyroid adj hormone adj receptor) or (pth adj receptor)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L31	82	((parathyroid adj hormone adj receptor) or (pth adj receptor)) same (agonist or antagonist) with (method or assay or screen\$3)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23

EAST Search History

L32	275	(parathyroid adj hormone adj receptor) or (pth adj receptor) with (agonist or antagonist)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L33	6	"6537965".pn. or "5494806".pn. or "200040698".pn.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L34	10	pth.ti. and receptor.ti.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L35	80	parathyroid.ti. and receptor.ti.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:23
L36	1484	(parathyroid near15 receptor) or (pthr-1 or pthr1 or hpthr-1 or hpthr1 or pthr or hpthr) or ((pth1 or pth-1 or hpt1 or hpt-1) near5 receptor)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:25
L37	76	L36 and (extracellular near30 (trunc\$7 or delet\$7))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:26
L38	65	L36 and receptor and (extracellular near15 (trunc\$7 or delet\$7))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:26
L39	49	L36 and receptor and (extracellular near5 (trunc\$7 or delet\$7))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/08/22 12:26

8/22/06

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STN SEARCH HISTORY

=> d his

(FILE 'HOME' ENTERED AT 10:55:59 ON 22 AUG 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, SCISEARCH, DISSABS, TOXCENTER' ENTERED AT
10:56:40 ON 22 AUG 2006

L1 708 S (GARDELLA T?/AU) OR (GARDELLA J?/AU)
L2 3076 S (KRONENBERG H?/AU) OR (KRONENBERG M?/AU)
L3 2810 S (POTTS J?/AU) OR (POTTS T?/AU)
L4 6279 S L1 OR L2 OR L3
L5 1448 S L4 AND PARATHYROID
L6 441 S L4 AND (PARATHYROID (5A) RECEPTOR)
L7 304 S (PTHR-1 OR PTHR1 OR HPTHR-1 OR HPTHR1)
L8 390 S ((PTH1 OR PTH-1) (2A)RECEPTOR)
L9 525 S (PTHR)
L10 9 S PTHR-DELNT
L11 5 S R-DELTA-NT
L12 1 S RDELTANT
L13 0 S R-DELTA-E1-G
L14 0 S R-DELTA-E1G
L15 0 S R-DELTAE1G
L16 0 S RDELTAE1G
L17 0 S RDELTAE1-G
L18 0 S RDELTA-E1-G
L19 21 S 26-181
L20 1221 S L7 OR L8 OR L9 OR L10 OR L11 OR L12 OR L19
L21 119 S L20 AND L4
L22 37 DUP REM L21 (82 DUPLICATES REMOVED)
L23 13 DUP REM L19 (8 DUPLICATES REMOVED)
L24 15 S L10 OR L11 OR L12
L25 4 DUP REM L24 (11 DUPLICATES REMOVED)
L26 8469 S (PARATHYROID) (15A) (RECEPTOR)
L27 77 S L26 AND (EXTRACELLULAR) AND (TRUNC?)
L28 26 DUP REM L27 (51 DUPLICATES REMOVED)
L29 1 S L26 AND ((EXTRACELLULAR) (5A) (TRUNC?))
L30 1200 S L7 OR L8 OR L9
L31 1 S L30 AND (EXTRACELLULAR (5A) (TRUNC? OR DELET?))

=> log y

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:02:23 ; Search time 266.154 Seconds
 (without alignments)
 9279.834 Million cell updates/sec

Title: US-09-869-565-1
 Perfect score: 1320
 Sequence: 1 atggggccgcggatcgc.....tcatgtgactggcactagg 1320

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:
 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PB_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1243.2	94.2	2051	2	US-07-864-475A-3	Sequence 3, Appli
2	1243.2	94.2	2051	2	US-08-468-249A-3	Sequence 3, Appli
3	966.8	73.2	1948	3	US-09-016-434-1253	Sequence 1253, Ap
4	965.2	73.1	2010	2	US-07-864-475A-4	Sequence 4, Appli
5	965.2	73.1	2010	2	US-08-468-249A-4	Sequence 4, Appli
6	959.6	72.7	1782	3	US-09-826-509-562	Sequence 562, App
7	691.6	52.4	1863	2	US-07-864-475A-2	Sequence 2, Appli
8	691.6	52.4	1863	2	US-08-468-249A-2	Sequence 2, Appli
9	681.2	51.6	1862	2	US-07-864-475A-1	Sequence 1, Appli
10	681.2	51.6	1862	2	US-08-468-249A-1	Sequence 1, Appli
11	554.6	42.0	1609	3	US-09-449-632-1	Sequence 1, Appli
12	387.4	29.3	2003	3	US-08-468-011A-1	Sequence 1, Appli
13	387.4	29.3	2003	3	US-09-236-468A-1	Sequence 1, Appli
14	387.4	29.3	2003	7	PCT-US95-07085-1	Sequence 1, Appli
15	387.4	29.3	2152	3	US-09-449-632-3	Sequence 3, Appli
16	387.4	29.3	2641	3	US-09-016-434-1463	Sequence 1463, Ap
17	385.8	29.2	1653	3	US-09-826-509-564	Sequence 564, App
18	196.6	14.9	1377	2	US-08-112-817C-1	Sequence 1, Appli
19	192.4	14.6	1374	3	US-09-826-509-578	Sequence 578, App
20	177.8	13.5	2025	3	US-09-016-434-1063	Sequence 1063, Ap
21	176.2	13.3	1401	3	US-09-826-509-506	Sequence 506, App
22	175.4	13.3	1578	3	US-09-016-434-1377	Sequence 1377, Ap
23	175.4	13.3	1809	2	US-08-453-956-24	Sequence 24, Appl
24	175.4	13.3	1809	2	US-08-086-631-24	Sequence 24, Appl
25	175.4	13.3	1809	2	US-08-452-930-24	Sequence 24, Appl
26	175.4	13.3	1809	7	PCT-US93-08174-24	Sequence 24, Appl
27	175.4	13.3	2034	3	US-10-010-065-5	Sequence 5, Appli
28	172.8	13.1	1323	3	US-09-826-509-566	Sequence 566, App
29	172.8	13.1	1616	3	US-09-016-434-1451	Sequence 1451, Ap
30	169.4	12.8	2616	3	US-09-016-434-1358	Sequence 1358, Ap
31	168.4	12.8	1944	3	US-10-010-065-1	Sequence 1, Appli
32	168.4	12.8	3066	2	US-08-142-439A-1	Sequence 1, Appli
33	168.4	12.8	3066	2	US-08-869-477-1	Sequence 1, Appli
34	166.2	12.6	1455	2	US-08-811-897A-31	Sequence 31, Appli
35	166.2	12.6	1455	2	US-08-855-213-31	Sequence 31, Appli
36	166.2	12.6	1455	3	US-09-201-474-31	Sequence 31, Appli
37	166.2	12.6	2730	2	US-08-811-897A-39	Sequence 39, Appli
38	166.2	12.6	2730	2	US-08-855-213-39	Sequence 39, Appli
39	166.2	12.6	2730	3	US-09-201-474-39	Sequence 39, Appli
40	158.8	12.0	1875	2	US-08-453-956-14	Sequence 14, Appli
41	158.8	12.0	1875	2	US-08-086-631-14	Sequence 14, Appli
42	158.8	12.0	1875	2	US-08-452-930-14	Sequence 14, Appli

43	158.8	12.0	1875	7	PCT-US93-08174-14	Sequence 14, Appl
44	151.4	11.5	1401	2	US-08-811-897A-32	Sequence 32, Appl
45	151.4	11.5	1401	2	US-08-855-213-32	Sequence 32, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:12:01 ; Search time 1863.59 Seconds
 (without alignments)
 8703.460 Million cell updates/sec

Title: US-09-869-565-1
 Perfect score: 1320
 Sequence: 1 atggggccgcggatcgc.....tcatgtgactggcactagg 1320

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_Main:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:
 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:
 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:
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 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
1	1243.2	94.2	2051	7	US-10-267-730-3	Sequence 3, Appli
2	1241.6	94.1	2065	8	US-10-152-319A-1741	Sequence 1741, Ap
3	1241.6	94.1	2065	16	US-11-036-196-1741	Sequence 1741, Ap
4	1236.4	93.7	2065	16	US-11-136-527-2547	Sequence 2547, Ap
5	1229.6	93.2	1776	3	US-09-943-446-3	Sequence 3, Appli
6	1146.4	86.8	1776	3	US-09-943-446-4	Sequence 4, Appli
7	1146.4	86.8	1776	3	US-09-943-446-5	Sequence 5, Appli
8	966.8	73.2	1948	6	US-10-225-567A-228	Sequence 228, App
9	966.8	73.2	1948	7	US-10-305-720-1253	Sequence 1253, Ap
10	966.8	73.2	1948	10	US-10-956-157-395	Sequence 395, App
11	966.8	73.2	2282	9	US-10-723-860-5567	Sequence 5567, Ap
12	965.2	73.1	2010	7	US-10-267-730-4	Sequence 4, Appli
13	965.2	73.1	2171	9	US-10-723-860-1005	Sequence 1005, Ap
14	959.6	72.7	1782	3	US-09-826-509-562	Sequence 562, App
15	959.6	72.7	1782	9	US-10-925-095-562	Sequence 562, App
16	958.2	72.6	1779	10	US-10-505-486-14	Sequence 14, Appli
17	902.2	68.3	2177	3	US-09-943-446-1	Sequence 1, Appli
18	899	68.1	1788	3	US-09-943-446-2	Sequence 2, Appli
19	758.4	57.5	2192	7	US-10-062-674-1564	Sequence 1564, Ap
20	691.6	52.4	1863	7	US-10-267-730-2	Sequence 2, Appli
21	681.2	51.6	1862	7	US-10-267-730-1	Sequence 1, Appli
22	610.8	46.3	681	8	US-10-332-859-229	Sequence 229, App
23	554.6	42.0	1609	7	US-10-372-095-1	Sequence 1, Appli
24	462.4	35.0	637	8	US-10-332-859-9	Sequence 9, Appli
25	393	29.8	600	16	US-11-136-527-6643	Sequence 6643, Ap
26	387.4	29.3	1896	7	US-10-295-027-523	Sequence 523, App
27	387.4	29.3	2003	3	US-09-996-569-1	Sequence 1, Appli
28	387.4	29.3	2003	9	US-10-921-218-1	Sequence 1, Appli
29	387.4	29.3	2152	7	US-10-372-095-3	Sequence 3, Appli
30	387.4	29.3	2641	6	US-10-225-567A-226	Sequence 226, App
31	387.4	29.3	2641	7	US-10-295-027-525	Sequence 525, App
32	387.4	29.3	2641	7	US-10-295-027-850	Sequence 850, App
33	387.4	29.3	2641	7	US-10-305-720-1463	Sequence 1463, Ap
34	387.4	29.3	2641	8	US-10-283-975A-70	Sequence 70, Appli
35	387.4	29.3	2641	9	US-10-723-860-2138	Sequence 2138, Ap
36	387.4	29.3	3071	9	US-10-723-860-6394	Sequence 6394, Ap

37	385.8	29.2	1653	3	US-09-826-509-564	Sequence 564, App
38	385.8	29.2	1653	9	US-10-925-095-564	Sequence 564, App
39	359	27.2	1977	16	US-11-136-527-2881	Sequence 2881, Ap
40	331.6	25.1	600	10	US-10-956-157-5630	Sequence 5630, Ap
41	331.6	25.1	600	13	US-11-060-756-1955	Sequence 1955, Ap
42	331.6	25.1	600	13	US-11-060-756-6227	Sequence 6227, Ap
43	328.6	24.9	343	7	US-10-062-674-392	Sequence 392, App
44	265	20.1	21704	7	US-10-017-161-709	Sequence 709, App
45	265	20.1	21704	7	US-10-292-798-621	Sequence 621, App

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:13:58 ; Search time 212.308 Seconds
 (without alignments)
 9503.772 Million cell updates/sec

Title: US-09-869-565-1
 Perfect score: 1320
 Sequence: 1 atggggccgcggatcg.....tcatgtgactggcactagg 1320

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2187952 seqs, 764289321 residues

Total number of hits satisfying chosen parameters: 4375904

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New:
 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:
 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:
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 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	965.2	73.1	2171	8	US-11-266-748A-31864	Sequence 31864, A
2	653.8	49.5	1037	8	US-11-266-748A-72888	Sequence 72888, A
3	653.8	49.5	1037	8	US-11-266-748A-107536	Sequence 107536,
c 4	653.8	49.5	1037	8	US-11-266-748A-125699	Sequence 125699,
5	637.6	48.3	1000	8	US-11-266-748A-115117	Sequence 115117,
c 6	637.6	48.3	1000	8	US-11-266-748A-157281	Sequence 157281,
7	637.6	48.3	1000	8	US-11-266-748A-220526	Sequence 220526,
8	637.6	48.3	1000	8	US-11-266-748A-283699	Sequence 283699,
c 9	637.6	48.3	1000	8	US-11-266-748A-335128	Sequence 335128,
10	637.6	48.3	1000	8	US-11-266-748A-393467	Sequence 393467,
c 11	637.6	48.3	1000	8	US-11-266-748A-464513	Sequence 464513,
12	326.2	24.7	651	8	US-11-266-748A-72887	Sequence 72887, A
13	326.2	24.7	651	8	US-11-266-748A-107535	Sequence 107535,
c 14	326.2	24.7	651	8	US-11-266-748A-125698	Sequence 125698,
c 15	315.6	23.9	718	6	US-10-473-173-255	Sequence 255, App
16	315	23.9	685	8	US-11-266-748A-365289	Sequence 365289,
c 17	315	23.9	685	8	US-11-266-748A-448668	Sequence 448668,
18	221.6	16.8	544	8	US-11-266-748A-264658	Sequence 264658,
c 19	221.6	16.8	544	8	US-11-266-748A-325175	Sequence 325175,
20	194	14.7	2771	8	US-11-266-748A-29527	Sequence 29527, A
21	177.8	13.5	2025	8	US-11-266-748A-31931	Sequence 31931, A
22	174.4	13.2	1323	8	US-11-266-748A-25118	Sequence 25118, A
23	168.4	12.8	1523	6	US-10-504-973-55	Sequence 55, Appl
24	158.6	12.0	1000	8	US-11-266-748A-115926	Sequence 115926,
c 25	158.6	12.0	1000	8	US-11-266-748A-158090	Sequence 158090,
26	158.6	12.0	1000	8	US-11-266-748A-396071	Sequence 396071,
c 27	158.6	12.0	1000	8	US-11-266-748A-467117	Sequence 467117,
28	147.6	11.2	1000	8	US-11-266-748A-284911	Sequence 284911,
c 29	147.6	11.2	1000	8	US-11-266-748A-336340	Sequence 336340,
30	147.6	11.2	1000	8	US-11-266-748A-395056	Sequence 395056,
c 31	147.6	11.2	1000	8	US-11-266-748A-466102	Sequence 466102,
32	138.2	10.5	1039	8	US-11-266-748A-352772	Sequence 352772,
33	138.2	10.5	1039	8	US-11-266-748A-384234	Sequence 384234,
c 34	138.2	10.5	1039	8	US-11-266-748A-436151	Sequence 436151,
c 35	132.6	10.0	986	8	US-11-266-748A-2319	Sequence 2319, Ap
36	132.6	10.0	986	8	US-11-266-748A-62948	Sequence 62948, A
c 37	132.6	10.0	986	8	US-11-266-748A-65780	Sequence 65780, A
38	128.4	9.7	1000	8	US-11-266-748A-393752	Sequence 393752,
c 39	128.4	9.7	1000	8	US-11-266-748A-464798	Sequence 464798,
40	127.4	9.7	1817	8	US-11-266-748A-59257	Sequence 59257, A
41	127.4	9.7	3958	8	US-11-266-748A-57216	Sequence 57216, A
42	120.8	9.2	1154	8	US-11-266-748A-367011	Sequence 367011,
43	120.8	9.2	1154	8	US-11-266-748A-388713	Sequence 388713,

c 44 120.8 9.2 1154 8 US-11-266-748A-450390 Sequence 450390,
c 45 116.6 8.8 908 8 US-11-266-748A-366994 Sequence 366994,

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:02:23 ; Search time 252.846 Seconds
 (without alignments)
 9279.834 Million cell updates/sec

Title: US-09-869-565-1_COPY_67_1320
 Perfect score: 1254
 Sequence: 1 tatgcgtggaggatattga.....tcatgtgactggcactagg 1254

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:
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 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
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 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1243.2	99.1	2051	2	US-07-864-475A-3	Sequence 3, Appli
2	1243.2	99.1	2051	2	US-08-468-249A-3	Sequence 3, Appli
3	966.8	77.1	1948	3	US-09-016-434-1253	Sequence 1253, Ap
4	965.2	77.0	2010	2	US-07-864-475A-4	Sequence 4, Appli
5	965.2	77.0	2010	2	US-08-468-249A-4	Sequence 4, Appli
6	959.6	76.5	1782	3	US-09-826-509-562	Sequence 562, App
7	691.6	55.2	1863	2	US-07-864-475A-2	Sequence 2, Appli
8	691.6	55.2	1863	2	US-08-468-249A-2	Sequence 2, Appli
9	681.2	54.3	1862	2	US-07-864-475A-1	Sequence 1, Appli
10	681.2	54.3	1862	2	US-08-468-249A-1	Sequence 1, Appli
11	554.6	44.2	1609	3	US-09-449-632-1	Sequence 1, Appli
12	387.4	30.9	2003	3	US-08-468-011A-1	Sequence 1, Appli
13	387.4	30.9	2003	3	US-09-236-468A-1	Sequence 1, Appli
14	387.4	30.9	2003	7	PCT-US95-07085-1	Sequence 1, Appli
15	387.4	30.9	2152	3	US-09-449-632-3	Sequence 3, Appli
16	387.4	30.9	2641	3	US-09-016-434-1463	Sequence 1463, Ap
17	385.8	30.8	1653	3	US-09-826-509-564	Sequence 564, App
18	196.6	15.7	1377	2	US-08-112-817C-1	Sequence 1, Appli
19	192.4	15.3	1374	3	US-09-826-509-578	Sequence 578, App
20	177.8	14.2	2025	3	US-09-016-434-1063	Sequence 1063, Ap
21	176.2	14.1	1401	3	US-09-826-509-506	Sequence 506, App
22	175.4	14.0	1578	3	US-09-016-434-1377	Sequence 1377, Ap
23	175.4	14.0	1809	2	US-08-453-956-24	Sequence 24, Appl
24	175.4	14.0	1809	2	US-08-086-631-24	Sequence 24, Appl
25	175.4	14.0	1809	2	US-08-452-930-24	Sequence 24, Appl
26	175.4	14.0	1809	7	PCT-US93-08174-24	Sequence 24, Appl
27	175.4	14.0	2034	3	US-10-010-065-5	Sequence 5, Appli
28	172.8	13.8	1323	3	US-09-826-509-566	Sequence 566, App
29	172.8	13.8	1616	3	US-09-016-434-1451	Sequence 1451, Ap
30	169.4	13.5	2616	3	US-09-016-434-1358	Sequence 1358, Ap
31	168.4	13.4	1944	3	US-10-010-065-1	Sequence 1, Appli
32	168.4	13.4	3066	2	US-08-142-439A-1	Sequence 1, Appli
33	168.4	13.4	3066	2	US-08-869-477-1	Sequence 1, Appli
34	166.2	13.3	1455	2	US-08-811-897A-31	Sequence 31, Appl
35	166.2	13.3	1455	2	US-08-855-213-31	Sequence 31, Appl
36	166.2	13.3	1455	3	US-09-201-474-31	Sequence 31, Appl
37	166.2	13.3	2730	2	US-08-811-897A-39	Sequence 39, Appl
38	166.2	13.3	2730	2	US-08-855-213-39	Sequence 39, Appl
39	166.2	13.3	2730	3	US-09-201-474-39	Sequence 39, Appl
40	158.8	12.7	1875	2	US-08-453-956-14	Sequence 14, Appl
41	158.8	12.7	1875	2	US-08-086-631-14	Sequence 14, Appl
42	158.8	12.7	1875	2	US-08-452-930-14	Sequence 14, Appl

43	158.8	12.7	1875	7	PCT-US93-08174-14	Sequence 14, Appl
44	151.4	12.1	1401	2	US-08-811-897A-32	Sequence 32, Appl
45	151.4	12.1	1401	2	US-08-855-213-32	Sequence 32, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:12:01 ; Search time 1770.41 Seconds
 (without alignments)
 8703.460 Million cell updates/sec

Title: US-09-869-565-1_COPY_67_1320
 Perfect score: 1254
 Sequence: 1 tatgcgctggaggatttga.....tcatgtgactggcactagg 1254

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_Main:
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 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1243.2	99.1	2051	7	US-10-267-730-3	Sequence 3, Appli
2	1241.6	99.0	2065	8	US-10-152-319A-1741	Sequence 1741, Ap
3	1241.6	99.0	2065	16	US-11-036-196-1741	Sequence 1741, Ap
4	1236.4	98.6	2065	16	US-11-136-527-2547	Sequence 2547, Ap
5	1229.6	98.1	1776	3	US-09-943-446-3	Sequence 3, Appli
6	1146.4	91.4	1776	3	US-09-943-446-4	Sequence 4, Appli
7	1146.4	91.4	1776	3	US-09-943-446-5	Sequence 5, Appli
8	966.8	77.1	1948	6	US-10-225-567A-228	Sequence 228, App
9	966.8	77.1	1948	7	US-10-305-720-1253	Sequence 1253, Ap
10	966.8	77.1	1948	10	US-10-956-157-395	Sequence 395, App
11	966.8	77.1	2282	9	US-10-723-860-5567	Sequence 5567, Ap
12	965.2	77.0	2010	7	US-10-267-730-4	Sequence 4, Appli
13	965.2	77.0	2171	9	US-10-723-860-1005	Sequence 1005, Ap
14	959.6	76.5	1782	3	US-09-826-509-562	Sequence 562, App
15	959.6	76.5	1782	9	US-10-925-095-562	Sequence 562, App
16	958.2	76.4	1779	10	US-10-505-486-14	Sequence 14, Appli
17	902.2	71.9	2177	3	US-09-943-446-1	Sequence 1, Appli
18	899	71.7	1788	3	US-09-943-446-2	Sequence 2, Appli
19	758.4	60.5	2192	7	US-10-062-674-1564	Sequence 1564, Ap
20	691.6	55.2	1863	7	US-10-267-730-2	Sequence 2, Appli
21	681.2	54.3	1862	7	US-10-267-730-1	Sequence 1, Appli
22	610.8	48.7	681	8	US-10-332-859-229	Sequence 229, App
23	554.6	44.2	1609	7	US-10-372-095-1	Sequence 1, Appli
24	462.4	36.9	637	8	US-10-332-859-9	Sequence 9, Appli
25	393	31.3	600	16	US-11-136-527-6643	Sequence 6643, Ap
26	387.4	30.9	1896	7	US-10-295-027-523	Sequence 523, App
27	387.4	30.9	2003	3	US-09-996-569-1	Sequence 1, Appli
28	387.4	30.9	2003	9	US-10-921-218-1	Sequence 1, Appli
29	387.4	30.9	2152	7	US-10-372-095-3	Sequence 3, Appli
30	387.4	30.9	2641	6	US-10-225-567A-226	Sequence 226, App
31	387.4	30.9	2641	7	US-10-295-027-525	Sequence 525, App
32	387.4	30.9	2641	7	US-10-295-027-850	Sequence 850, App
33	387.4	30.9	2641	7	US-10-305-720-1463	Sequence 1463, Ap
34	387.4	30.9	2641	8	US-10-283-975A-70	Sequence 70, Appl
35	387.4	30.9	2641	9	US-10-723-860-2138	Sequence 2138, Ap
36	387.4	30.9	3071	9	US-10-723-860-6394	Sequence 6394, Ap

37	385.8	30.8	1653	3	US-09-826-509-564	Sequence 564, App
38	385.8	30.8	1653	9	US-10-925-095-564	Sequence 564, App
39	359	28.6	1977	16	US-11-136-527-2881	Sequence 2881, Ap
40	331.6	26.4	600	10	US-10-956-157-5630	Sequence 5630, Ap
41	331.6	26.4	600	13	US-11-060-756-1955	Sequence 1955, Ap
42	331.6	26.4	600	13	US-11-060-756-6227	Sequence 6227, Ap
43	328.6	26.2	343	7	US-10-062-674-392	Sequence 392, App
44	265	21.1	21704	7	US-10-017-161-709	Sequence 709, App
45	265	21.1	21704	7	US-10-292-798-621	Sequence 621, App

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2006, 17:13:58 ; Search time 201.692 Seconds
 (without alignments)
 9503.772 Million cell updates/sec

Title: US-09-869-565-1_COPY_67_1320
 Perfect score: 1254
 Sequence: 1 tatgcgctggaggatttga.....tcatgtgactggcactagg 1254

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2187952 seqs, 764289321 residues

Total number of hits satisfying chosen parameters: 4375904

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_New:
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 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:
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 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	965.2	77.0	2171	8	US-11-266-748A-31864	Sequence 31864, A
2	653.8	52.1	1037	8	US-11-266-748A-72888	Sequence 72888, A
3	653.8	52.1	1037	8	US-11-266-748A-107536	Sequence 107536,
c 4	653.8	52.1	1037	8	US-11-266-748A-125699	Sequence 125699,
5	637.6	50.8	1000	8	US-11-266-748A-115117	Sequence 115117,
c 6	637.6	50.8	1000	8	US-11-266-748A-157281	Sequence 157281,
7	637.6	50.8	1000	8	US-11-266-748A-220526	Sequence 220526,
8	637.6	50.8	1000	8	US-11-266-748A-283699	Sequence 283699,
c 9	637.6	50.8	1000	8	US-11-266-748A-335128	Sequence 335128,
10	637.6	50.8	1000	8	US-11-266-748A-393467	Sequence 393467,
c 11	637.6	50.8	1000	8	US-11-266-748A-464513	Sequence 464513,
12	326.2	26.0	651	8	US-11-266-748A-72887	Sequence 72887, A
13	326.2	26.0	651	8	US-11-266-748A-107535	Sequence 107535,
c 14	326.2	26.0	651	8	US-11-266-748A-125698	Sequence 125698,
c 15	315.6	25.2	718	6	US-10-473-173-255	Sequence 255, App
16	315	25.1	685	8	US-11-266-748A-365289	Sequence 365289,
c 17	315	25.1	685	8	US-11-266-748A-448668	Sequence 448668,
18	221.6	17.7	544	8	US-11-266-748A-264658	Sequence 264658,
c 19	221.6	17.7	544	8	US-11-266-748A-325175	Sequence 325175,
20	194	15.5	2771	8	US-11-266-748A-29527	Sequence 29527, A
21	177.8	14.2	2025	8	US-11-266-748A-31931	Sequence 31931, A
22	174.4	13.9	1323	8	US-11-266-748A-25118	Sequence 25118, A
23	168.4	13.4	1523	6	US-10-504-973-55	Sequence 55, Appl
24	158.6	12.6	1000	8	US-11-266-748A-115926	Sequence 115926,
c 25	158.6	12.6	1000	8	US-11-266-748A-158090	Sequence 158090,
26	158.6	12.6	1000	8	US-11-266-748A-396071	Sequence 396071,
c 27	158.6	12.6	1000	8	US-11-266-748A-467117	Sequence 467117,
28	147.6	11.8	1000	8	US-11-266-748A-284911	Sequence 284911,
c 29	147.6	11.8	1000	8	US-11-266-748A-336340	Sequence 336340,
30	147.6	11.8	1000	8	US-11-266-748A-395056	Sequence 395056,
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32	138.2	11.0	1039	8	US-11-266-748A-352772	Sequence 352772,
33	138.2	11.0	1039	8	US-11-266-748A-384234	Sequence 384234,
c 34	138.2	11.0	1039	8	US-11-266-748A-436151	Sequence 436151,
c 35	132.6	10.6	986	8	US-11-266-748A-2319	Sequence 2319, Ap
36	132.6	10.6	986	8	US-11-266-748A-62948	Sequence 62948, A
c 37	132.6	10.6	986	8	US-11-266-748A-65780	Sequence 65780, A
38	128.4	10.2	1000	8	US-11-266-748A-393752	Sequence 393752,
c 39	128.4	10.2	1000	8	US-11-266-748A-464798	Sequence 464798,
40	127.4	10.2	1817	8	US-11-266-748A-59257	Sequence 59257, A
41	127.4	10.2	3958	8	US-11-266-748A-57216	Sequence 57216, A
42	120.8	9.6	1154	8	US-11-266-748A-367011	Sequence 367011,
43	120.8	9.6	1154	8	US-11-266-748A-388713	Sequence 388713,

c 44 120.8 9.6 1154 8 US-11-266-748A-450390 Sequence 450390,
c 45 116.6 9.3 908 8 US-11-266-748A-366994, Sequence 366994,

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:23:07 ; Search time 37.4469 Seconds
 (without alignments)
 1016.794 Million cell updates/sec

Title: US-09-869-565-2
 Perfect score: 2283
 Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLLQEGWETVM 435

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2195	96.1	591	1	US-08-468-249A-20	Sequence 20, Appl
2	2008	88.0	593	2	US-09-631-603-21	Sequence 21, Appl
3	2002	87.7	593	1	US-08-468-249A-21	Sequence 21, Appl
4	2002	87.7	593	2	US-09-826-509-563	Sequence 563, App
5	1710	74.9	585	1	US-08-142-439A-6	Sequence 6, Appli
6	1710	74.9	585	1	US-08-142-551B-125	Sequence 125, App
7	1710	74.9	585	1	US-08-869-477-6	Sequence 6, Appli
8	1710	74.9	585	1	US-08-468-249A-19	Sequence 19, Appl
9	1551	67.9	515	1	US-08-468-249A-18	Sequence 18, Appl
10	1465	64.2	536	2	US-09-449-632-2	Sequence 2, Appli
11	1130	49.5	542	2	US-09-449-632-4	Sequence 4, Appli
12	1068	46.8	575	2	US-09-449-632-5	Sequence 5, Appli
13	1050.5	46.0	550	2	US-09-631-603-20	Sequence 20, Appl
14	1044.5	45.8	550	2	US-09-826-509-565	Sequence 565, App
15	1036	45.4	541	2	US-08-468-011A-2	Sequence 2, Appli
16	1036	45.4	541	2	US-09-236-468A-2	Sequence 2, Appli
17	1036	45.4	541	5	PCT-US95-07085-2	Sequence 2, Appli
18	960.5	42.1	207	2	US-08-811-519-31	Sequence 31, Appl
19	776	34.0	459	2	US-09-694-519-4	Sequence 4, Appli
20	775.5	34.0	1324	1	US-08-811-897A-56	Sequence 56, Appl
21	775.5	34.0	1324	2	US-09-201-474-56	Sequence 56, Appl
22	773.5	33.9	444	2	US-09-694-519-6	Sequence 6, Appli
23	772	33.8	459	2	US-09-694-519-3	Sequence 3, Appli
24	772	33.8	459	2	US-09-694-519-8	Sequence 8, Appli
25	762.5	33.4	458	1	US-08-112-817C-2	Sequence 2, Appli
26	762.5	33.4	458	2	US-09-694-519-5	Sequence 5, Appli
27	762.5	33.4	458	2	US-09-694-519-7	Sequence 7, Appli
28	757.5	33.2	449	1	US-08-142-439A-5	Sequence 5, Appli
29	757.5	33.2	449	1	US-08-869-477-5	Sequence 5, Appli
30	752.5	33.0	457	2	US-09-631-603-23	Sequence 23, Appl
31	752.5	33.0	457	2	US-09-694-519-1	Sequence 1, Appli
32	747	32.7	440	2	US-09-631-603-22	Sequence 22, Appl
33	746.5	32.7	457	2	US-09-826-509-579	Sequence 579, App
34	741	32.5	460	2	US-09-694-519-2	Sequence 2, Appli
35	738	32.3	440	2	US-09-826-509-567	Sequence 567, App
36	718	31.4	447	2	US-09-694-519-9	Sequence 9, Appli
37	687	30.1	448	1	US-08-811-897A-22	Sequence 22, Appl
38	687	30.1	448	1	US-08-855-213-22	Sequence 22, Appl
39	687	30.1	448	2	US-09-201-474-22	Sequence 22, Appl
40	687	30.1	468	2	US-09-631-603-19	Sequence 19, Appl
41	687	30.1	525	1	US-08-811-897A-23	Sequence 23, Appl
42	687	30.1	525	1	US-08-855-213-23	Sequence 23, Appl
43	687	30.1	525	2	US-09-201-474-23	Sequence 23, Appl
44	684	30.0	448	1	US-08-811-897A-18	Sequence 18, Appl
45	684	30.0	448	1	US-08-855-213-18	Sequence 18, Appl

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:39:27 ; Search time 132.86 Seconds
 (without alignments)
 1516.626 Million cell updates/sec

Title: US-09-869-565-2
 Perfect score: 2283
 Sequence: 1 MGAARIAPSLALLCCPVLSEASGSARPPPLLQEGWETVM 435

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_Main:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	96.1	591	4 US-10-267-730-20	Sequence 20, Appl
2	2187	95.8	591	3 US-09-943-446-7	Sequence 7, Appl
3	2146	94.0	591	3 US-09-943-446-8	Sequence 8, Appl
4	2008	88.0	593	3 US-09-943-446-9	Sequence 9, Appl
5	2008	88.0	593	4 US-10-225-567A-229	Sequence 229, App
6	2008	88.0	593	5 US-10-723-860-1006	Sequence 1006, Ap
7	2008	88.0	593	5 US-10-505-486-13	Sequence 13, Appl
8	2008	88.0	593	6 US-11-199-821-10	Sequence 10, Appl
9	2002	87.7	593	3 US-09-826-509-563	Sequence 563, App
10	2002	87.7	593	4 US-10-267-730-21	Sequence 21, Appl
11	2002	87.7	593	5 US-10-925-095-563	Sequence 563, App
12	1957	85.7	595	3 US-09-943-446-6	Sequence 6, Appl
13	1710	74.9	585	4 US-10-267-730-19	Sequence 19, Appl
14	1698	74.4	964	4 US-10-017-161-710	Sequence 710, App
15	1698	74.4	964	4 US-10-292-798-622	Sequence 622, App
16	1551	67.9	515	4 US-10-267-730-18	Sequence 18, Appl
17	1465	64.2	536	4 US-10-372-095-2	Sequence 2, Appl
18	1130	49.5	542	4 US-10-372-095-4	Sequence 4, Appl
19	1068	46.8	575	4 US-10-372-095-5	Sequence 5, Appl
20	1050.5	46.0	550	4 US-10-225-567A-227	Sequence 227, App
21	1050.5	46.0	550	4 US-10-295-027-526	Sequence 526, App
22	1050.5	46.0	550	4 US-10-295-027-851	Sequence 851, App
23	1050.5	46.0	550	5 US-10-723-860-2139	Sequence 2139, Ap
24	1050.5	46.0	561	4 US-10-295-027-524	Sequence 524, App
25	1044.5	45.8	550	3 US-09-826-509-565	Sequence 565, App
26	1044.5	45.8	550	5 US-10-925-095-565	Sequence 565, App
27	1036	45.4	541	3 US-09-996-569-2	Sequence 2, Appli
28	1036	45.4	541	5 US-10-921-218-2	Sequence 2, Appli
29	1028.5	45.1	550	4 US-10-014-162-110	Sequence 110, App
30	1011.5	44.3	546	4 US-10-014-162-109	Sequence 109, App
31	776	34.0	459	4 US-10-831-393-4	Sequence 4, Appli
32	775.5	34.0	1324	3 US-09-935-371-56	Sequence 56, Appli
33	773.5	33.9	444	4 US-10-831-393-6	Sequence 6, Appli
34	772	33.8	459	4 US-10-831-393-3	Sequence 3, Appli
35	772	33.8	459	4 US-10-831-393-8	Sequence 8, Appli
36	762.5	33.4	458	4 US-10-831-393-5	Sequence 5, Appli
37	762.5	33.4	458	4 US-10-831-393-7	Sequence 7, Appli
38	757.5	33.2	449	4 US-10-051-874-68	Sequence 68, Appli
39	752.5	33.0	457	4 US-10-225-567A-469	Sequence 469, App
40	752.5	33.0	457	4 US-10-292-798-618	Sequence 618, App
41	752.5	33.0	457	4 US-10-831-393-1	Sequence 1, Appli
42	752.5	33.0	457	6 US-11-199-821-13	Sequence 13, Appli
43	747	32.7	440	4 US-10-292-798-608	Sequence 608, App
44	747	32.7	440	4 US-10-051-874-64	Sequence 64, Appli
45	747	32.7	440	4 US-10-051-874-65	Sequence 65, Appli

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:40:02 ; Search time 21.5448 Seconds
 (without alignments)
 1333.463 Million cell updates/sec

Title: US-09-869-565-2
 Perfect score: 2283
 Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLLQEGWETVM 435

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:
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 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	476	20.8	461	6 US-10-505-928-282	Sequence 282, App
2	457.5	20.0	375	7 US-11-358-841-10	Sequence 10, Appl
3	457.5	20.0	415	7 US-11-358-841-9	Sequence 9, Appl
4	455	19.9	309	7 US-11-358-841-13	Sequence 13, Appl
5	453.5	19.9	375	7 US-11-358-841-3	Sequence 3, Appl
6	453.5	19.9	415	7 US-11-358-841-1	Sequence 1, Appl
7	429	18.8	444	7 US-11-358-841-2	Sequence 2, Appl
8	382.5	16.8	401	7 US-11-358-841-4	Sequence 4, Appl
9	381.5	16.7	240	7 US-11-358-841-14	Sequence 14, Appl
10	313.5	13.7	284	6 US-10-504-973-16	Sequence 16, Appl
11	296.5	13.0	341	7 US-11-358-841-7	Sequence 7, Appl
12	287.5	12.6	319	7 US-11-358-841-12	Sequence 12, Appl
13	285.5	12.5	356	7 US-11-358-841-36	Sequence 36, Appl
14	283.5	12.4	370	7 US-11-358-841-6	Sequence 6, Appl
15	281.5	12.3	320	7 US-11-358-841-32	Sequence 32, Appl
16	219	9.6	327	7 US-11-358-841-37	Sequence 37, Appl
17	219	9.6	339	7 US-11-358-841-35	Sequence 35, Appl
18	213	9.3	283	6 US-10-504-973-13	Sequence 13, Appl
19	200.5	8.8	742	7 US-11-289-102-241	Sequence 241, App
20	200.5	8.8	786	6 US-10-504-973-31	Sequence 31, Appl
21	190.5	8.3	1403	6 US-10-505-928-471	Sequence 471, App
22	187	8.2	400	6 US-10-504-973-17	Sequence 17, Appl
23	176	7.7	528	6 US-10-196-749-490	Sequence 490, App
24	175.5	7.7	801	6 US-10-504-973-38	Sequence 38, Appl
25	166	7.3	695	7 US-11-293-697-3126	Sequence 3126, Ap
26	163.5	7.2	687	7 US-11-218-716-8	Sequence 8, Appl
27	156.5	6.9	693	6 US-10-505-928-678	Sequence 678, App
28	156.5	6.9	693	7 US-11-218-716-2	Sequence 2, Appl
29	156.5	6.9	693	7 US-11-218-716-4	Sequence 4, Appl
30	156.5	6.9	693	7 US-11-218-716-6	Sequence 6, Appl
31	149.5	6.5	504	6 US-10-539-228-334	Sequence 334, App
32	149.5	6.5	504	6 US-10-539-228-336	Sequence 336, App
33	144.5	6.3	510	6 US-10-539-228-338	Sequence 338, App
34	144.5	6.3	510	6 US-10-539-228-340	Sequence 340, App
35	134.5	5.9	687	7 US-11-341-947-2	Sequence 2, Appl
36	134.5	5.9	687	7 US-11-218-716-10	Sequence 10, Appl
37	119.5	5.2	686	6 US-10-539-228-331	Sequence 331, App
38	101.5	4.4	352	6 US-10-505-928-745	Sequence 745, App
39	101.5	4.4	352	6 US-10-511-937-2486	Sequence 2486, App
40	101.5	4.4	352	6 US-10-511-937-2935	Sequence 2935, App
41	101.5	4.4	352	6 US-10-511-937-3010	Sequence 3010, App
42	97.5	4.3	335	7 US-11-056-355B-57140	Sequence 57140, A
43	97.5	4.3	407	7 US-11-056-355B-57139	Sequence 57139, A
44	96.5	4.2	197	7 US-11-056-355B-35249	Sequence 35249, A

45 95.5 4.2 362 7 US-11-175-714-130

Sequence 130, App

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:23:07 ; Search time 35.5531 Seconds
(without alignments)
1016.794 Million cell updates/sec

Title: US-09-869-565-2_COPY_23_435
Perfect score: 2175
Sequence: 1 YALEVFDRLGMIYTVGYSMS.....EASGSARPPPLLQEGWETVM 413

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2160	99.3	591	1	US-08-468-249A-20	Sequence 20, Appl
2	1981	91.1	593	2	US-09-631-603-21	Sequence 21, Appl
3	1975	90.8	593	1	US-08-468-249A-21	Sequence 21, Appl
4	1975	90.8	593	2	US-09-826-509-563	Sequence 563, App
5	1702.5	78.3	585	1	US-08-142-439A-6	Sequence 6, Appli
6	1702.5	78.3	585	1	US-08-142-551B-125	Sequence 125, App
7	1702.5	78.3	585	1	US-08-869-477-6	Sequence 6, Appli
8	1702.5	78.3	585	1	US-08-468-249A-19	Sequence 19, Appl
9	1543.5	71.0	515	1	US-08-468-249A-18	Sequence 18, Appl
10	1465	67.4	536	2	US-09-449-632-2	Sequence 2, Appli
11	1130	52.0	542	2	US-09-449-632-4	Sequence 4, Appli
12	1068	49.1	575	2	US-09-449-632-5	Sequence 5, Appli
13	1050.5	48.3	550	2	US-09-631-603-20	Sequence 20, Appl
14	1044.5	48.0	550	2	US-09-826-509-565	Sequence 565, App
15	1036	47.6	541	2	US-08-468-011A-2	Sequence 2, Appli
16	1036	47.6	541	2	US-09-236-468A-2	Sequence 2, Appli
17	1036	47.6	541	5	PCT-US95-07085-2	Sequence 2, Appli
18	960.5	44.2	207	2	US-08-811-519-31	Sequence 31, Appl
19	776	35.7	459	2	US-09-694-519-4	Sequence 4, Appli
20	775.5	35.7	1324	1	US-08-811-897A-56	Sequence 56, Appl
21	775.5	35.7	1324	2	US-09-201-474-56	Sequence 56, Appl
22	773.5	35.6	444	2	US-09-694-519-6	Sequence 6, Appli
23	772	35.5	459	2	US-09-694-519-3	Sequence 3, Appli
24	772	35.5	459	2	US-09-694-519-8	Sequence 8, Appli
25	762.5	35.1	458	1	US-08-112-817C-2	Sequence 2, Appli
26	762.5	35.1	458	2	US-09-694-519-5	Sequence 5, Appli
27	762.5	35.1	458	2	US-09-694-519-7	Sequence 7, Appli
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29	755.5	34.7	449	1	US-08-869-477-5	Sequence 5, Appli
30	752.5	34.6	457	2	US-09-631-603-23	Sequence 23, Appl
31	752.5	34.6	457	2	US-09-694-519-1	Sequence 1, Appli
32	747	34.3	440	2	US-09-631-603-22	Sequence 22, Appl
33	746.5	34.3	457	2	US-09-826-509-579	Sequence 579, App
34	741	34.1	460	2	US-09-694-519-2	Sequence 2, Appli
35	738	33.9	440	2	US-09-826-509-567	Sequence 567, App
36	718	33.0	447	2	US-09-694-519-9	Sequence 9, Appli
37	687	31.6	448	1	US-08-811-897A-22	Sequence 22, Appl
38	687	31.6	448	1	US-08-855-213-22	Sequence 22, Appl
39	687	31.6	448	2	US-09-201-474-22	Sequence 22, Appl
40	687	31.6	468	2	US-09-631-603-19	Sequence 19, Appl
41	687	31.6	525	1	US-08-811-897A-23	Sequence 23, Appl
42	687	31.6	525	1	US-08-855-213-23	Sequence 23, Appl
43	687	31.6	525	2	US-09-201-474-23	Sequence 23, Appl
44	684	31.4	448	1	US-08-811-897A-18	Sequence 18, Appl
45	684	31.4	448	1	US-08-855-213-18	Sequence 18, Appl

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:39:27 ; Search time 126.14 Seconds
 (without alignments)
 1516.626 Million cell updates/sec

Title: US-09-869-565-2_COPY_23_435
 Perfect score: 2175
 Sequence: 1 YALEVFDRILGMIYTVGYSMS.....EASGSARPPPLLQEGWETVM 413

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_Main:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2160	99.3	591	4	US-10-267-730-20	Sequence 20, Appl
2	2152	98.9	591	3	US-09-943-446-7	Sequence 7, Appl
3	2115	97.2	591	3	US-09-943-446-8	Sequence 8, Appl
4	1981	91.1	593	3	US-09-943-446-9	Sequence 9, Appl
5	1981	91.1	593	4	US-10-225-567A-229	Sequence 229, App
6	1981	91.1	593	5	US-10-723-860-1006	Sequence 1006, Ap
7	1981	91.1	593	5	US-10-505-486-13	Sequence 13, Appl
8	1981	91.1	593	6	US-11-199-821-10	Sequence 10, Appl
9	1975	90.8	593	3	US-09-826-509-563	Sequence 563, App
10	1975	90.8	593	4	US-10-267-730-21	Sequence 21, Appl
11	1975	90.8	593	5	US-10-925-095-563	Sequence 563, App
12	1930	88.7	595	3	US-09-943-446-6	Sequence 6, Appl
13	1702.5	78.3	585	4	US-10-267-730-19	Sequence 19, Appl
14	1698	78.1	964	4	US-10-017-161-710	Sequence 710, App
15	1698	78.1	964	4	US-10-292-798-622	Sequence 622, App
16	1543.5	71.0	515	4	US-10-267-730-18	Sequence 18, Appl
17	1465	67.4	536	4	US-10-372-095-2	Sequence 2, Appli
18	1130	52.0	542	4	US-10-372-095-4	Sequence 4, Appli
19	1068	49.1	575	4	US-10-372-095-5	Sequence 5, Appli
20	1050.5	48.3	550	4	US-10-225-567A-227	Sequence 227, App
21	1050.5	48.3	550	4	US-10-295-027-526	Sequence 526, App
22	1050.5	48.3	550	4	US-10-295-027-851	Sequence 851, App
23	1050.5	48.3	550	5	US-10-723-860-2139	Sequence 2139, Ap
24	1050.5	48.3	561	4	US-10-295-027-524	Sequence 524, App
25	1044.5	48.0	550	3	US-09-826-509-565	Sequence 565, App
26	1044.5	48.0	550	5	US-10-925-095-565	Sequence 565, App
27	1036	47.6	541	3	US-09-996-569-2	Sequence 2, Appli
28	1036	47.6	541	5	US-10-921-218-2	Sequence 2, Appli
29	1028.5	47.3	550	4	US-10-014-162-110	Sequence 110, App
30	1011.5	46.5	546	4	US-10-014-162-109	Sequence 109, App
31	776	35.7	459	4	US-10-831-393-4	Sequence 4, Appli
32	775.5	35.7	1324	3	US-09-935-371-56	Sequence 56, Appli
33	773.5	35.6	444	4	US-10-831-393-6	Sequence 6, Appli
34	772	35.5	459	4	US-10-831-393-3	Sequence 3, Appli
35	772	35.5	459	4	US-10-831-393-8	Sequence 8, Appli
36	762.5	35.1	458	4	US-10-831-393-5	Sequence 5, Appli
37	762.5	35.1	458	4	US-10-831-393-7	Sequence 7, Appli
38	755.5	34.7	449	4	US-10-051-874-68	Sequence 68, Appli
39	752.5	34.6	457	4	US-10-225-567A-469	Sequence 469, App
40	752.5	34.6	457	4	US-10-292-798-618	Sequence 618, App
41	752.5	34.6	457	4	US-10-831-393-1	Sequence 1, Appli
42	752.5	34.6	457	6	US-11-199-821-13	Sequence 13, Appli
43	747	34.3	440	4	US-10-292-798-608	Sequence 608, App
44	747	34.3	440	4	US-10-051-874-64	Sequence 64, Appli
45	747	34.3	440	4	US-10-051-874-65	Sequence 65, Appli

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OM protein - protein search, using sw model

Run on: July 26, 2006, 21:40:02 ; Search time 20.4552 Seconds
 (without alignments)
 1333.463 Million cell updates/sec

Title: US-09-869-565-2_COPY_23_435
 Perfect score: 2175
 Sequence: 1 YALEVFDRLGMIYTVGYSMS.....EASGSARPPPLLQEGWETVM 413

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	476	21.9	461	6	US-10-505-928-282	Sequence 282, App
2	455	20.9	309	7	US-11-358-841-13	Sequence 13, Appl
3	455	20.9	375	7	US-11-358-841-10	Sequence 10, Appl
4	455	20.9	415	7	US-11-358-841-9	Sequence 9, Appli
5	452	20.8	375	7	US-11-358-841-3	Sequence 3, Appli
6	452	20.8	415	7	US-11-358-841-1	Sequence 1, Appli
7	427.5	19.7	444	7	US-11-358-841-2	Sequence 2, Appli
8	381.5	17.5	240	7	US-11-358-841-14	Sequence 14, Appli
9	381	17.5	401	7	US-11-358-841-4	Sequence 4, Appli
10	313.5	14.4	284	6	US-10-504-973-16	Sequence 16, Appli
11	295	13.6	341	7	US-11-358-841-7	Sequence 7, Appli
12	285	13.1	319	7	US-11-358-841-12	Sequence 12, Appli
13	283	13.0	356	7	US-11-358-841-36	Sequence 36, Appli
14	282	13.0	370	7	US-11-358-841-6	Sequence 6, Appli
15	279	12.8	320	7	US-11-358-841-32	Sequence 32, Appli
16	216.5	10.0	327	7	US-11-358-841-37	Sequence 37, Appli
17	216.5	10.0	339	7	US-11-358-841-35	Sequence 35, Appli
18	213	9.8	283	6	US-10-504-973-13	Sequence 13, Appli
19	196.5	9.0	742	7	US-11-289-102-241	Sequence 241, App
20	196.5	9.0	786	6	US-10-504-973-31	Sequence 31, Appli
21	190.5	8.8	1403	6	US-10-505-928-471	Sequence 471, App
22	179	8.2	400	6	US-10-504-973-17	Sequence 17, Appli
23	172.5	7.9	528	6	US-10-196-749-490	Sequence 490, App
24	171.5	7.9	801	6	US-10-504-973-38	Sequence 38, Appli
25	166	7.6	695	7	US-11-293-697-3126	Sequence 3126, Ap
26	163.5	7.5	687	7	US-11-218-716-8	Sequence 8, Appli
27	156.5	7.2	693	6	US-10-505-928-678	Sequence 678, App
28	156.5	7.2	693	7	US-11-218-716-2	Sequence 2, Appli
29	156.5	7.2	693	7	US-11-218-716-4	Sequence 4, Appli
30	156.5	7.2	693	7	US-11-218-716-6	Sequence 6, Appli
31	149.5	6.9	504	6	US-10-539-228-334	Sequence 334, App
32	149.5	6.9	504	6	US-10-539-228-336	Sequence 336, App
33	144.5	6.6	510	6	US-10-539-228-338	Sequence 338, App
34	144.5	6.6	510	6	US-10-539-228-340	Sequence 340, App
35	134.5	6.2	687	7	US-11-341-947-2	Sequence 2, Appli
36	134.5	6.2	687	7	US-11-218-716-10	Sequence 10, Appli
37	119.5	5.5	686	6	US-10-539-228-331	Sequence 331, App
38	101.5	4.7	352	6	US-10-505-928-745	Sequence 745, App
39	101.5	4.7	352	6	US-10-511-937-2486	Sequence 2486, Ap
40	101.5	4.7	352	6	US-10-511-937-2935	Sequence 2935, Ap
41	101.5	4.7	352	6	US-10-511-937-3010	Sequence 3010, Ap
42	96.5	4.4	197	7	US-11-056-3558-35249	Sequence 35249, A
43	95.5	4.4	362	7	US-11-175-714-130	Sequence 130, App
44	94.5	4.3	525	6	US-10-449-902-43532	Sequence 43532, A

45 93 4.3 335 7 US-11-056-355B-57140 Sequence 57140, A